



#5

4-31452A.ST25.txt
SEQUENCE LISTING

<110> Novartis AG
<120> Adenovirus particles with mutagenized fiber proteins
<130> 4-31452A
<140> US 09/870,203
<141> 2001-05-30
<160> 43
<170> PatentIn version 3.1
<210> 1
<211> 1746
<212> DNA
<213> Human adenovirus type 5
<220>
<221> CDS
<222> (1)..(1746)
<223>

<400> 1
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

1

4-31452A.ST25.txt

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 92	1
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40	2
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88	2
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36	3
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84	3
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32	4
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 80	4
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	

4-31452A.ST25.txt

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

200

205

gct cct ttg cat gta àca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

265

270

```

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag      8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
      275              280              285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac      9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
      290              295              300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag      9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305              310              315              320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata      10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
      325              330              335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca      10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
      340              345              ~      350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat      11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
      355              360              365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac      11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

```

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

4-31452A.ST25.txt

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa 17
46
Tyr Ile Ala Gln Glu

580

<210> 2

<211> 581

<212> PRT

<213> Human adenovirus type 5

<400> 2

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 3
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)
<223>

<220>
<221> mutation
<222> (1222)..(1227)
<223>

<400> 3
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

1

4-31452A.ST25.txt

35	40	45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc			1
92			
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu			
50	55	60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc			2
40			
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser			
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac			2
88			
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			
	85	90	95
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta			3
36			
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
	100	105	110
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc			3
84			
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
	115	120	125
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att			4
32			
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
	130	135	140
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa			4
80			

4-31452A.ST25.txt

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8

4-31452A.ST25.txt

16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag

8

64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac

9

12

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag

9

60

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata

10

08

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca

10

56

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat

11

04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12
48

405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

4-31452A.ST25.txt

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 88	14
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly	
485 490 495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 36	15
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
500 505 510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 84	15
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
515 520 525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 32	16
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 80	16
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555 560	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 28	17
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	
565 570 575	
tac att gcc caa gaa taa 46	17
Tyr Ile Ala Gln Glu	
580	

<210> 4
 <211> 581
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein.
 <400> 4

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

4-31452A.ST25.txt

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525

4-31452A.ST25.txt

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 5
<211> 1740
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le
otides corresponding to amino acids 441(V) & 442(K) of wild-typ
e
fiber were deleted.

<220>
<221> CDS
<222> (1)..(1740)
<223>

<400> 5
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 44 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser 35 40 45	1
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu 50 55 60	1
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser 65 70 75 80	2
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn 85 90 95	2
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100 105 110	3
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115 120 125	3
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	4

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

4-31452A.ST25.txt

245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt			8
16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag			8
64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac			9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag			9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata			10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca			10
56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat			11
04			

4-31452A.ST25.txt

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13
44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13
92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14

4-31452A.ST25.txt

40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg

14

88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt

15

36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta

15

84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act

16

32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac

16

80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att

17

28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa
40
Ala Gln Glu

<210> 6
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted.

<400> 6

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr		
		115					120					125					
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile		
	130					135					140						
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln		
145					150					155					160		
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr		
			165						170					175			
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu		
			180					185					190				
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly		
	195					200						205					
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr		
	210					215					220						
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr		
225					230					235					240		
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala		
			245					250						255			
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val		
		260						265					270				
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln		
		275					280					285					
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn		
	290					295					300						

4-31452A.ST25.txt

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
485 490 495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
 500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
 515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
 530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
 545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
 565 570 575

Ala Gln Glu

<210> 7
 <211> 1740
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb
 in
 ation of the mutant fiber encoded in Seq ID: #3 & 5.

<220>
 <221> CDS
 <222> (1)..(1740)
 <223>

<400> 7
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

4-31452A.ST25.txt

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

4-31452A.ST25.txt

225	230	235	240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca				7
68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala				
	245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt				8
16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val				
	260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag				8
64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln				
	275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac				9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn				
	290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag				9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu				
305	310	315	320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata				10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile				
	325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca				10
56				

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13
44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13

4-31452A.ST25.txt

92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat

14

40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg

14

88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt

15

36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta

15

84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act

16

32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac

16

80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

4-31452A.ST25.txt

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa

17

40

Ala Gln Glu

<210> 8

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb
in

ation of the mutant fiber encoded in Seq ID: #3 & 5.

<400> 8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
 435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
 450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

4-31452A.ST25.txt

<400> 9

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

4-31452A.ST25.txt

210	215	220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			7
225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			7
	245	250	255
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			8
	260	265	270
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			8
	275	280	285
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			9
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			9
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08			10

4-31452A.ST25.txt

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct 13

4-31452A.ST25.txt

44
Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
435 440 445

gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga 13
92
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga 14
40
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt 14
88
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa 15
36
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15
84
Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16
32
Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
530 535 540

4-31452A.ST25.txt

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545 550 555 560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565 570 575

att gcc caa gaa taa 17
43

Ile Ala Gln Glu

580

<210> 10
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le
otides corresponding to amino acid 441(V) of wild-type fiber wa
s
deleted.

<400> 10

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

4-31452A.ST25.txt

Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
50						55					60				
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70					75					80
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn
				85					90					95	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu
			100					105					110		
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr
		115					120					125			
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile
	130					135					140				
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln
145					150					155					160
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr
				165					170					175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
			180					185					190		
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly
		195					200					205			
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
	210					215					220				
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr
225					230					235					240

4-31452A.ST25.txt

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

4-31452A.ST25.txt

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
530 535 540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
565 570 575

Ile Ala Gln Glu
580

<210> 11

<211> 1743

<212> DNA

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le

otides corresponding to amino acid 442(K) of wild-type fiber was
deleted.

<220>

<221> CDS

<222> (1)..(1743)

<223>

<400> 11

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

2

4-31452A.ST25.txt

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg

6

4-31452A.ST25.txt

24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
72

6

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
20

7

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca
68

7

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt
16

8

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag
64

8

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac
12

9

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

4-31452A.ST25.txt

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt ggc agt ttg gct cca ata tct 13
44
Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser

435

440

445

gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga 13
92
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly

450

455

460

gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga 14
40
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg

465

470

475

480

aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt 14
88
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe

485

490

495

atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa 15
36
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys

500

505

510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15
84
Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16
32

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545

550

555

560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565

570

575

att gcc caa gaa taa

17

43

Ile Ala Gln Glu

580

<210> 12

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le
otides corresponding to amino acid 442(K) of wild-type fiber wa
s
deleted.

<400> 12

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

4-31452A.ST25.txt

Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro			
			20					25					30					
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser			
		35					40					45						
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu			
	50					55					60							
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser			
65					70					75					80			
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn			
				85					90					95				
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu			
			100					105					110					
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr			
		115					120					125						
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile			
	130					135					140							
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln			
145					150					155					160			
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr			
				165					170					175				
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu			
			180					185					190					
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly			
		195					200					205						

4-31452A.ST25.txt

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

4-31452A.ST25.txt

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465 470 475 480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
530 535 540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
565 570 575

Ile Ala Gln Glu
580

<210> 13
 <211> 1746
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
 <221> CDS
 <222> (1)..(1746)
 <223>

<220>
 <221> mutation
 <222> (1321)..(1326)
 <223>

<400> 13
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
 44
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
 92
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40	2
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88	2
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36	3
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84	3
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32	4
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 80	4
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 28	5
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac			9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag			9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata			10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca			10
56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat			11
04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac			11
52 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act			12
00			

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Page 60

4-31452A.ST25.txt

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa

15

84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac

16

32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc

16

80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca

17

28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

17

46

Tyr Ile Ala Gln Glu

580

<210> 14

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<400> 14

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

4-31452A.ST25.txt

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

4-31452A.ST25.txt

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu
580

<210> 15
<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)
<223>

<220>
<221> mutation
<222> (1378)..(1380)
<223>

<400> 15
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

1

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 92	1
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 40	2
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 88	2
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 36	3
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 84	3
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 32	4
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 80	4
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	

145	150	155	160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act				5
28				
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr				
	165	170	175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg				5
76				
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu				
	180	185	190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg				6
24				
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly				
	195	200	205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act				6
72				
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr				
	210	215	220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act				7
20				
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr				
225	230	235	240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca				7
68				
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala				
	245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt				8
16				
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val				

4-31452A.ST25.txt

260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			8
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			9
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			9
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			10
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			10
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			11
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 52			11

4-31452A.ST25.txt

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
 ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
 48
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415
 aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
 96
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430
 ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
 44
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445
 tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat 13
 92
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
 450 455 460
 gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
 40
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480
 aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14

4-31452A.ST25.txt

88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15

84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16

32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16

80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17

28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

46

Tyr Ile Ala Gln Glu

17

580

4-31452A.ST25.txt

<210> 16
 <211> 581
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein.
 <400> 16

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145		150		155		160									
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr
				165					170					175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
				180				185					190		
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly
		195					200					205			
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
	210					215					220				
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr
225					230					235					240
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala
				245					250					255	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val
			260					265					270		
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln
		275					280					285			
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn
	290					295					300				
Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu
305					310					315					320
Val	Asn	Leu	Ser	Thr	Ala	Lys	Gly	Leu	Met	Phe	Asp	Ala	Thr	Ala	Ile
				325					330					335	
Ala	Ile	Asn	Ala	Gly	Asp	Gly	Leu	Glu	Phe	Gly	Ser	Pro	Asn	Ala	Pro

340

345

350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
 450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575

Tyr Ile Ala Gln Glu
 580

<210> 17
 <211> 1740
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
 le
 otides corresponding to amino acids 509(G) & 510(K) of wild-typ
 e
 fiber were deleted.

<220>
 <221> CDS
 <222> (1)..(1740)
 <223>

<400> 17
 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

4-31452A.ST25.txt

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

140

4-31452A.ST25.txt

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 80 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	4
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 28 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	5
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	5
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	6
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	6
210 215 220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	7
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	7
245 250 255	

4-31452A.ST25.txt

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	8
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	8
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	9
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	9
305 310 315 320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	10
325 330 335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	10
340 345 350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	11

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

4-31452A.ST25.txt

465	470	475	480	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga				14
88				
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				
	485	490	495	
ttt atg cct aac cta tca gct tat cca aaa tct cac act gcc aaa agt				15
36				
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser				
	500	505	510	
aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta				15
84				
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val				
	515	520	525	
aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act				16
32				
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr				
	530	535	540	
cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac				16
80				
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn				
545	550	555	560	
tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att				17
28				
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile				
	565	570	575	
gcc caa gaa taa				17
40				

Ala Gln Glu

<210> 18

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted.

<400> 18

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

4-31452A.ST25.txt

Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	115	120	125	
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	130	135	140	
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	145	150	155	160
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	165	170	175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	180	185	190	
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	195	200	205	
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr	210	215	220	
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr	225	230	235	240
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala	245	250	255	
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val	260	265	270	
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	275	280	285	
Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	290	295	300	

4-31452A.ST25.txt

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

4-31452A.ST25.txt

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 19
<211> 1740
<212> DNA
<213> Artificial Sequence

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le
otides corresponding to amino acids 538(G) & 539(T) of wild-typ
e
fiber were deleted.

<220>
<221> CDS
<222> (1)..(1740)
<223>

<400> 19
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

4-31452A.ST25.txt

225	230	235	240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca				7
68 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala				
	245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt				8
16 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val				
	260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag				8
64 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln				
	275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac				9
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn				
	290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag				9
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu				
305	310	315	320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata				10
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile				
	325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca				10
56				

4-31452A.ST25.txt

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13

4-31452A.ST25.txt

92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac cag gaa aca gga gac aca act 16
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

4-31452A.ST25.txt

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa 17
40
Ala Gln Glu

<210> 20
<211> 579
<212> PRT
<213> Artificial Sequence

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc
le
otides corresponding to amino acids 538(G) & 539(T) of wild-typ
e
fiber were deleted.

<400> 20

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

4-31452A.ST25.txt

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

4-31452A.ST25.txt

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

4-31452A.ST25.txt

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)
<223>

<400> 21

accacaccag ctccagaggc taactgtaga ctaaattgc
38

<210> 22
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)
<223>

<400> 22
gcatttagtc tacagtttagc ctctggagct ggtgtggt
38

<210> 23
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(38)
<223>

<400> 23
acagtttcag ttttggccgg cagtttggt ccaatatc
38

<210> 24
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(38)

<223>

<400> 24

gatattggag ccaaactgcc ggccaaaact gaaactgt
38

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 25

acagtttcag ttttggctaa aggcagtttg gctcca
36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 26

tggagccaaa ctgccttttag ccaaaactga aactgt

36

<210> 27
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<220>
 <221> primer_bind
 <222> (1)..(36)
 <223>

<400> 27
 gtttcagttt tggctgttgg cagtttggct ccaata
 36

<210> 28
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<220>
 <221> primer_bind
 <222> (1)..(36)
 <223>

<400> 28
 tattggagcc aaactgccaa cagccaaaac tgaaac
 36

<210> 29
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 29

gtttcagttt tggctgctgc aggcagtttg gctcca
36

<210> 30

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 30

tggagccaaa ctgcctgcag cagccaaaac tgaaac
36

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(36)

<223>

<400> 31

gctcatctta ttatagaatt cgacgaaaat ggagtg
36

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)
<223>

<400> 32
cactccattt tcgtcgaatt ctataataag atgagc
36

<210> 33
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(39)
<223>

<400> 33
gcttatccaa aatctcacac tgccaaaagt aacattgtc
39

<210> 34
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(39)

<223>

<400> 34

gacaatgtta cttttggcag tgtgagattt tggataagc

39

<210> 35

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(35)

<223>

<400> 35

ctaaccatta cactaaacca ggaaacagga gacac

35

<210> 36

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(35)

<223>

<400> 36

gtgtctcctg tttcctgggt tagtgtaatg gttag

35

<210> 37
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 37
ataagatttg acgaaactgg agtgctacta aac
33

<210> 38
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 38
gttttagtagc actccagttt cgtcaaattct tat
33

<210> 39
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>

<221> primer_bind
<222> (1)..(33)
<223>

<400> 39
tttgacgaaa atggacacct actaaacaat tcc
33

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 40
ggaattgttt agtaggtgtc cagtttcgtc aaa
33

<210> 41
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(33)
<223>

<400> 41
aacctatcag cttatgcaaa atctcacggt aaa
33

<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(32)
<223>

<400> 42
tttaccgtga gattttgcat aagctgatag gt
32

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> cRGD consensus sequence

<400> 43

His Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5 10